

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2005, 20:11:47 ; Search time 176 Seconds
(without alignments)
2129.784 Million cell updates/sec

Title: US-10-768-030-1
Perfect score: 3761
Sequence: 1 MVRSGNKAALVCLMDVQFTM.....GDTAAVFEGGVDDLLDMI 732

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3756	99.9	731	1 KU86 HUMAN	P13010 h atp-depen
2	2971	79.0	732	2 Q60449	Q60449 cricetus
3	2971	79.0	732	2 Q60530	Q60530 mesocricetu
4	2939	78.1	732	2 Q80U71	Q80U71 mus musculu
5	2937	78.1	731	2 Q8K1K7	Q8K1K7 mus musculu
6	2932	78.0	732	2 Q9R169	Q9R169 mus musculu
7	2922	77.7	732	2 Q6P7P8	Q6P7P8 rattus norv
8	2893	76.9	732	1 KU86 MOUSE	P27641 mus musculu
9	2865.5	76.2	708	2 Q8C4N6	Q8C4N6 mus musculu
10	2748	73.1	683	2 Q8V1B0	Q8V1B0 rattus norv
11	2339	62.2	726	2 Q6DD59	Q6DD59 xenopus lae
12	2327	61.9	726	2 Q9W627	Q9W627 xenopus lae
13	1065	28.3	283	2 Q9C1U5	Q9C1U5 mus musculu
14	694	18.5	138	2 Q6U1L6	Q6U1L6 pan troglod
15	688	18.3	138	2 Q6U1L5	Q6U1L5 macaca mula
16	585	15.6	683	2 Q8S563	Q8S563 medicago tr
17	569	15.1	686	2 Q8S562	Q8S562 phaseolus v
18	540.5	14.4	593	2 Q7Q190	Q7Q190 anopheles g
19	525	14.0	680	2 Q9FQ09	Q9FQ09 arabidopsis
20	525	14.0	688	2 Q751P6	Q751P6 oryza sativ
21	496	13.2	663	2 Q9C723	Q9C723 arabidopsis
22	459	12.2	707	2 Q9LNF5	Q9LNF5 arabidopsis
23	418.5	11.1	661	2 Q7RX73	Q7RX73 neurospora
24	402.5	10.7	145	2 Q90Z03	Q90Z03 oryza lat
25	344	9.1	726	2 Q6C7B9	Q6C7B9 yarrowia li
26	342	9.1	695	2 Q9HGW8	Q9HGW8 achizosacch
27	318.5	8.5	699	2 Q8MSN8	Q8MSN8 drosophila
28	318.5	8.5	699	2 Q9NGX6	Q9NGX6 drosophila
29	316.5	8.4	699	2 Q9I7M8	Q9I7M8 drosophila
30	309.5	8.2	904	2 Q9NK79	Q9NK79 drosophila
31	294.5	7.8	728	2 Q21829	Q21829 caenorhabdi

RESULT 1

ID	KU86 HUMAN	STANDARD;	PRT;	731 AA.
AC	P13010;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	ATP-dependent DNA helicase II, 80 kDa subunit (Lupus Ku autoantigen protein p86) (Ku80) (86 kDa subunit of Ku antigen) (Thyroid-lupus autoantigen) (TLAA) (CTC box binding factor 85 kDa subunit) (CTCBF) (CTC85) (Nuclear factor IV) (DNA-repair protein XRCC5).			
GN	Name=XRCC5; Synonyms=G22P2;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 3-21.			
RX	MEDLINE=89340410; PubMed=2760028;			
RA	Yanava M., Wen J., Ayala A., Cook R.;			
RT	"cDNA-derived amino acid sequence of the 86-kDa subunit of the Ku antigen."			
RL	J. Biol. Chem. 264:13407-13411(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90175380; PubMed=2308937;			
RA	Mimori T., Ohosone Y., Hama N., Suwa A., Akizuki M., Homma M., Griffith A.J., Hardin J.A.;			
RT	"Isolation and characterization of cDNA encoding the 80-kDa subunit protein of the human autoantigen Ku (p70/p80) recognized by autoantibodies from patients with scleroderma-polymyositis overlap syndrome."			
RL	Proc. Natl. Acad. Sci. U.S.A. 87:1777-1781(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins B., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg K.H., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haefl F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fabsy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfield G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			

ALIGNMENTS

32	233	6.2	325	2	Q751P5	Q751P5 oryza sativ
33	203	5.4	40	2	Q9UCQ1	Q9UCQ1 homo sapien
34	180	4.8	585	2	Q6CCK2	Q6CCK2 yarrowia li
35	173	4.6	608	2	Q8QX7	Q8QX7 mus musculu
36	172	4.6	615	2	Q6FN20	Q6FN20 candida gla
37	172	4.6	645	2	Q7SA95	Q7SA95 neurospora
38	171	4.5	723	2	Q6EXN4	Q6EXN4 debaryomyce
39	170	4.5	608	1	KU70 MOUSE	P23475 mus musculu
40	161.5	4.3	600	1	KU70 RHIAF	Q26228 thipicephal
41	157.5	4.2	634	2	Q95PL8	Q95PL8 trypanosoma
42	157.5	4.2	1370	2	Q6A078	Q6A078 mus musculu
43	152	4.0	3065	2	Q70WN3	Q70WN3 peru tomato
44	151	4.0	608	2	Q9QVN9	Q9QVN9 cricetus
45	150.5	4.0	629	1	KU80 YEAST	Q04437 saccharomyc

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OM protein - protein search, using sw model

Run on: August 17, 2005, 20:13:52 ; Search time 44 Seconds
(without alignments)
1600.697 Million cell updates/sec

Title: US-10-768-030-1
Perfect score: 3761
Sequence: 1 MVRSGNKAAYVLCMDVGFMT.....GDTAAVPEEGDVLDDMI 732

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: Pirl: *
2: Pirl: *
3: Pirl: *
4: Pirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3761	100.0	732	2 A32626	Ku antigen 80K cha
2	2971	79.0	732	2 J06099	Ku autoantigen 86k
3	2893	76.9	732	2 S26303	Ku autoantigen 80K
4	459	12.2	707	2 G96520	protein P21D18.26
5	294.5	7.8	728	2 S43606	R07E5.8 protein (c
6	175	4.7	595	2 A43534	Lupus autoantigen
7	161.5	4.3	600	2 S65788	Ku antigen 70K cha
8	150.5	4.0	629	2 S54567	hypothetical prote
9	146.5	3.9	1055	2 H64577	type I restriction
10	145	3.9	607	2 T40906	probable ATP-depen
11	143.5	3.8	1356	2 S32763	kinectin 1 - huma
12	142	3.8	602	2 S24591	DNA-binding factor
13	141	3.7	1939	2 T18372	repeat organellar
14	138	3.7	1300	2 I53799	CGI protein - huma
15	135.5	3.6	2094	2 S33124	tpi protein - huma
16	135	3.6	1496	2 T00499	probable retroelem
17	134	3.6	1927	2 G84585	cag pathogenicity
18	134	3.6	2166	2 G70163	hypothetical prote
19	132.5	3.5	871	2 B37035	DNA polymerase I,
20	132	3.5	1440	2 T33813	hypothetical prote
21	132	3.5	1642	2 T08880	NMDA receptor-bind
22	131	3.5	609	2 A30894	70K thyroid autoan
23	131	3.5	950	2 A71655	hypothetical prote
24	129	3.4	607	2 D86305	hypothetical prote
25	129	3.4	1087	2 T30330	gelsolin-related p
26	129	3.4	1538	2 T29095	cardiac muscle fac
27	127.5	3.4	990	2 H88733	protein P32E10.3 I
28	127	3.4	904	2 T03806	hypothetical prote
29	127	3.4	1837	2 T41023	probable nuclear p

ALIGNMENTS

RESULT 1

A32626

Ku antigen 80K chain - human

N;Alternate names: CTC 85 protein; DNA-dependent ATPase 83k chain; Ku autoantigen; nucl

C;Species: Homo sapiens (man)

C;Date: 21-May-1990 #sequence revision 21-May-1990 #text change 09-Jul-2004

C;Accession: A35051; A32626; J03022; A39235; C42397; S54273; A54197

R;Mimori, T.; Ohosone, Y.; Hama, N.; Suwa, A.; Akizuki, M.; Homma, M.; Griffith, A.J.;

Proc. Natl. Acad. Sci. U.S.A. 87, 1777-1781, 1990

A;Title: Isolation and characterization of cDNA encoding the 80-kDa subunit protein of

lap syndrome.

A;Reference number: A35051; MUID:90175380; PMID:2308937

A;Accession: A35051

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-732 <MIM>

A;Cross-references: UNIPROT:P13010; GB:M30938; NID:G186793; PIDN:AAA36154.1; PID:G30709

R;Yanava, M.; Wen, J.; Ayala, A.; Cook, R.

J. Biol. Chem. 264, 13407-13411, 1989

A;Title: cDNA-derived amino acid sequence of the 86-kDa subunit of the Ku antigen.

A;Reference number: A32626; MUID:89340410; PMID:2760028

A;Accession: A32626

A;Molecule type: mRNA

A;Residues: 1-732 <YAN>

A;Cross-references: GB:J04977; NID:G186791; PIDN:AAA59475.1; PID:G307093

R;Stuiver, M.H.; Coenjaerts, F.E.J.; van der Vliet, P.C.

J. Exp. Med. 172, 1049-1054, 1990

A;Title: The autoantigen Ku is indistinguishable from NF IV, a protein forming multimer

A;Reference number: J03022; MUID:91011245; PMID:2212941

A;Accession: J03022

A;Molecule type: mRNA

A;Residues: 105-732 <STU>

A;Experimental source: strain Ntera 2D1

R;Knoth, M.W.; Gunderson, S.I.; Thompson, N.E.; Strasheim, L.A.; Burgess, R.R.

J. Biol. Chem. 265, 17911-17920, 1990

A;Title: Purification and characterization of proximal sequence element-binding protein

man UI promoter.

A;Reference number: A39235; MUID:91009259; PMID:2211668

A;Accession: A39235

A;Molecule type: protein

A;Residues: 2-12, 'X', 14-22 <KNU>

R;Wedrychowski, A.; Henzel, W.; Huston, L.; Paslidis, N.; Ellerson, D.; McRae, M.; Seon

J. Biol. Chem. 267, 4533-4540, 1992

A;Title: Identification of proteins binding to interferon-inducible transcriptional enh

A;Reference number: A42397; MUID:92165807; PMID:1537839

A;Accession: A42397

A;Status: preliminary

A;Molecule type: protein

A;Residues: 526-565 <WED>

A;Experimental source: K562 cells

A;Note: sequence extracted from NCBI backbone (NCBIP:85281)

R;Genersch, E.; Beckerskorn, C.; Lottapeich, F.; Herzog, C.; Kuehn, K.; Poeschl, E.

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OM protein - protein search, using sw model

Run on: August 17, 2005, 20:15:42 ; Search time 166 Seconds

(without alignments)
1726.753 Million cell updates/sec

Title: US-10-768-030-1

Perfect score: 3761

Sequence: 1 MYRSGNKAAYVLCMDVGFTM.....GDTAAVFEGDVEDLDDMI 732

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3761	100.0	732	14 US-10-097-340-363	Sequence 363, App
2	3761	100.0	732	15 US-10-116-275-169	Sequence 169, App
3	3761	100.0	732	16 US-10-408-765A-1124	Sequence 1124, App
4	3761	100.0	732	17 US-10-768-030-1	Sequence 1, Appl
5	3761	100.0	741	9 US-09-833-790-432	Sequence 432, App
6	3756	99.9	731	14 US-10-160-748-7	Sequence 7, Appl
7	2971	79.0	732	14 US-10-160-748-4	Sequence 4, Appl
8	2971	79.0	732	14 US-10-160-748-5	Sequence 5, Appl
9	2893	76.9	732	14 US-10-160-748-6	Sequence 6, Appl
10	2545.5	67.7	521	9 US-09-805-020-37	Sequence 38, Appl
11	2530	67.3	497	9 US-09-805-020-37	Sequence 37, Appl

12	545	14.5	721	15	US-10-425-114-62759	Sequence 62759, A
13	543	14.4	681	14	US-10-160-748-2	Sequence 2, Appl
14	537	14.3	681	16	US-10-425-115-357314	Sequence 357314, A
15	489	13.0	132	9	US-09-925-301-1530	Sequence 1530, App
16	390.5	10.4	631	16	US-10-437-963-133099	Sequence 133099, A
17	339	9.0	64	9	US-09-864-761-35456	Sequence 35456, A
18	294.5	7.8	728	15	US-10-369-493-5694	Sequence 5694, App
19	293	7.8	56	9	US-09-864-761-37896	Sequence 37896, A
20	288	7.7	55	9	US-09-864-761-34694	Sequence 34694, A
21	288	7.7	55	9	US-09-864-761-36475	Sequence 36475, A
22	288	7.7	55	9	US-09-864-761-42907	Sequence 42907, A
23	283	7.5	292	16	US-10-425-115-357315	Sequence 357315, A
24	239	6.4	379	15	US-10-424-599-188014	Sequence 188014, A
25	221	5.9	44	9	US-09-864-761-35402	Sequence 35402, A
26	219	5.8	42	14	US-10-189-437-548	Sequence 548, App
27	184	4.9	673	15	US-10-369-493-13409	Sequence 13409, A
28	171	4.5	638	15	US-10-369-493-3523	Sequence 3523, App
29	169.5	4.5	190	15	US-10-425-114-52621	Sequence 52621, A
30	159	4.2	136	16	US-10-767-701-54545	Sequence 54545, A
31	151	4.0	166	15	US-10-424-599-278336	Sequence 278336, A
32	147	3.9	142	15	US-10-424-599-167597	Sequence 167597, A
33	146.5	3.9	1055	10	US-09-882-227-596	Sequence 596, App
34	142	3.8	602	15	US-10-369-493-1922	Sequence 1922, App
35	141	3.7	1939	17	US-10-732-923-3340	Sequence 3340, App
36	140	3.7	5317	16	US-10-668-767-59	Sequence 59, Appl
37	139	3.7	1861	14	US-10-032-585-7646	Sequence 7646, App
38	138	3.7	1300	16	US-10-408-765A-257	Sequence 257, App
39	136.5	3.6	113	16	US-10-767-701-54564	Sequence 54564, A
40	136.5	3.6	2654	14	US-10-227-610-2	Sequence 2, Appl
41	136	3.6	730	16	US-10-437-963-179929	Sequence 179929, A
42	136	3.6	799	15	US-10-369-493-20654	Sequence 20654, A
43	135.5	3.6	684	16	US-10-425-115-357245	Sequence 357245, A
44	135.5	3.6	841	16	US-10-425-115-231005	Sequence 231005, A
45	134.5	3.6	715	16	US-10-408-765A-2096	Sequence 2096, App

ALIGNMENTS

RESULT 1

US-10-097-340-363
Sequence 363, Application US/10097340
Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVAPU
APPLICANT: Sebastian HOESCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISSEY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VIBBY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. EAST, Jr.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHMANDT
APPLICANT: Xumei ZHAO
APPLICANT: Karen GLATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, Assessment, Prevention, and Therapy of Ovarian Cancer
FILE OF INVENTION: MRI-030
CURRENT FILING DATE: 2002-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-09-26

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OM protein - protein search, using sw model

Run on: August 17, 2005, 20:11:01 ; Search time 24 Seconds
(without alignments)
2276.796 Million cell updates/sec

Title: US-10-768-030-1
Perfect score: 3761
Sequence: 1 MVRSGNKAADVLCMDVGTFT.....GDTAAVFEFGDVLDDMI 732

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgm2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgm2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/5A COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/5B COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/PTCUS COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3761	100.0	732	4	US-09-569-037-7
2	3761	100.0	732	4	US-09-949-016-7000
3	3761	100.0	743	4	US-09-949-016-11192
4	3756	99.9	731	4	US-10-160-748-7
5	3730	99.2	820	3	US-09-173-914-2
6	2971	79.0	732	4	US-10-160-748-4
7	2971	79.0	732	4	US-10-160-748-5
8	2893	76.9	732	4	US-10-160-748-6
9	700	18.6	137	4	US-09-513-999C-5706
10	543	14.4	681	4	US-10-160-748-2
11	394	10.5	78	4	US-09-569-037-16
12	314.5	8.4	77	4	US-09-569-037-17
13	314.5	8.4	77	4	US-09-569-037-18
14	294.5	7.8	728	4	US-09-569-037-8
15	174	4.6	34	4	US-09-569-037-11
16	161.5	4.3	600	4	US-09-569-037-4
17	150.5	4.0	629	4	US-09-569-037-9
18	141	3.7	602	4	US-09-569-037-6
19	139.5	3.7	531	4	US-09-248-796A-19139
20	138	3.7	1307	3	US-09-949-016-7561
21	137.5	3.7	650	3	US-09-385-801-2
22	135.5	3.6	2186	4	US-09-949-016-10828
23	135.5	3.6	2349	4	US-09-538-092-914
24	131	3.5	608	3	US-08-360-107A-126
25	131	3.5	609	4	US-09-569-037-2
26	130	3.5	1010	3	US-09-134-001C-5178
27	129.5	3.4	607	3	US-08-486-099-116

28	129.5	3.4	607	3	US-08-484-223B-116	Sequence 116, App
29	129.5	3.4	607	3	US-08-919-597-116	Sequence 116, App
30	129.5	3.4	607	3	US-08-475-668A-116	Sequence 116, App
31	129.5	3.4	607	3	US-08-485-551A-116	Sequence 116, App
32	129.5	3.4	607	3	US-08-471-913A-116	Sequence 116, App
33	129.5	3.4	607	3	US-08-485-264A-116	Sequence 116, App
34	129.5	3.4	607	3	US-08-474-349A-116	Sequence 116, App
35	129.5	3.4	607	4	US-08-470-896-116	Sequence 116, App
36	129.5	3.4	607	4	US-08-485-546A-116	Sequence 116, App
37	129.5	3.4	607	4	US-08-487-266A-116	Sequence 2, Appli
38	127	3.4	904	3	US-09-198-484-2	Sequence 11, Appli
39	126	3.4	3878	4	US-09-914-259-11	Sequence 16013, A
40	125	3.3	862	4	US-09-248-796A-16013	Sequence 8, Appli
41	122	3.2	1234	4	US-09-592-054-8	Sequence 9959, Ap
42	121	3.2	1346	4	US-09-949-016-9959	Sequence 14866, A
43	120	3.2	636	4	US-09-248-796A-14866	Sequence 4, Appli
44	119.5	3.2	495	3	US-09-198-484-4	Sequence 936, App
45	119.5	3.2	2871	4	US-09-538-092-936	

ALIGNMENTS

RESULT 1
US-09-569-037-7
; Sequence 7, Application US/09569037
; Patent No. 6753151
; GENERAL INFORMATION:
; APPLICANT: Jackson, Stephen P
; APPLICANT: Gell, David A
; TITLE OF INVENTION: Interactions of Ku polypeptides and applications
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 620-100
; CURRENT APPLICATION NUMBER: US/09/569,037
; CURRENT FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: PCT/GB00/01245
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: GB 9907687.9
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 7
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-037-7

Query Match	100.0%;	Score 3761;	DB 4;	Length 732;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 732;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MVRSGNKAADVLCMDVGTFTMSNIPGIESPPEQAKVITMFVQVQVFAENKDEIALVLF 60		
Db	1	MVRSGNKAADVLCMDVGTFTMSNIPGIESPPEQAKVITMFVQVQVFAENKDEIALVLF 60		
Qy	61	TGTDNPLSGDQYONITVHRHMLPFDLLESTKIQSGQADFDALIVSMVLIQH 120		
Db	61	TGTDNPLSGDQYONITVHRHMLPFDLLESTKIQSGQADFDALIVSMVLIQH 120		
Qy	121	ETICKKFKKHIEFTDLSRFSKQDIIITHSLKKCDISIQFFLPFSLGKEDSGDRGD 180		
Db	121	ETICKKFKKHIEFTDLSRFSKQDIIITHSLKKCDISIQFFLPFSLGKEDSGDRGD 180		
Qy	181	GPFFLGHGHPFLKIGITEQOQKGLIYKVMVMSLEGEDGLDDEIYFSFESLKLKCVFKKI 240		
Db	181	GPFFLGHGHPFLKIGITEQOQKGLIYKVMVMSLEGEDGLDDEIYFSFESLKLKCVFKKI 240		
Qy	241	ERHSIHWPCLRTIGSNLSIRIAAKSILQBRVKKTTVVDATKTKKEDIQKETYVCLNDD 300		
Db	241	ERHSIHWPCLRTIGSNLSIRIAAKSILQBRVKKTTVVDATKTKKEDIQKETYVCLNDD 300		
Qy	301	DETVLKEEDITQGFYGSDIVPFRKVBEOOMKYSKGFVSGCKSSQVQRRFFMGNQ 360		

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OM protein - protein search, using sw model

Run on: August 17, 2005, 20:08:01 ; Search time 165 Seconds
(without alignments)
1715.810 Million cell updates/sec

Title: US-10-768-030-1

Perfect score: 3761

Sequence: 1 MVRSGNKAAYVLCMDVGTW.....GDTAAVPEGGVDLLDMI 732

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3761	100.0	732	5	ABG96452 Human ova
2	3761	100.0	732	7	ADJ69318 Human hea
3	3761	100.0	732	8	ADP43915 Human DNA
4	3761	100.0	732	8	ADQ14382 Human lup
5	3761	100.0	732	8	ABM80379 Tumour-as
6	3761	100.0	732	8	ADR97394 Human XRC
7	3761	100.0	732	8	ADS14356 Human lup
8	3761	100.0	741	5	AU69427 Lung smal
9	3756	99.9	731	8	ADJ66474 ATP-depen
10	3754	99.8	732	8	ADR41763 Protein s
11	3730	99.2	820	4	AAB66590 Human KAR
12	3688	98.1	732	4	AAB29307 Human Ku8
13	3354	89.2	757	4	ABG08315 Novel hum
14	3221	85.6	628	6	ABU07475 Protein d
15	2893	76.9	732	2	AAW40496 Mouse XRC
16	2545.5	67.7	521	5	ABG79671 Tumour in
17	2530	67.3	497	5	ABG79670 Mouse XRC
18	2454	65.2	644	2	AAW40497 Novel hum
19	1784	47.4	384	4	ABG08312 Novel hum
20	1034.5	27.5	710	4	ABG08311 Novel hum
21	926.5	24.6	210	6	ABG99983 Human nov
22	700	18.6	137	3	AAQ01625 Human sec
23	658.5	17.5	138	4	ABG08310 Novel hum
24	543	14.4	681	3	AAB19283 Amino aci
25	489	13.0	132	3	AAB44085 Human can

ALIGNMENTS

RESULT 1

ABG96452

ID ABG96452 standard; protein; 732 AA.

XX AC ABG96452;

DT 11-DEC-2002 (first entry)

DE Human ovarian cancer marker M480.

XX Human; ovarian cancer; marker; cancer; familial history; brain disorder;

KW central nervous system disorder; bacterial meningitis; viral meningitis;
KW Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
KW brain herniation; inflammation; encephalitis; testicular disorder;
KW nontuberculous granulomatous orchitis; connective tissue disorder;
KW heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
KW histological type; carcinogenic; ovarian cancer marker.

XX Homo sapiens.

DN WO200271928-A2.

XX 19-SEP-2002.

PD 14-MAR-2002; 2002WO-US007826.

XX 14-MAR-2001; 2001US-0276025P.

PR 14-MAR-2001; 2001US-0276026P.

PR 10-AUG-2001; 2001US-0311732P.

PR 19-SEP-2001; 2001US-0323580P.

PR 26-SEP-2001; 2001US-0324967P.

PR 26-SEP-2001; 2001US-0325102P.

PR 26-SEP-2001; 2001US-0325149P.

(MILL-) MILLENNIUM PHARM INC.

Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
Meyers RE, Morrissy WP, Olandt PJ, Sen A, Vieby PO, Mills GB;
Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;
WPI; 2002-723277/78.
N-PSDB; ABS76552.

XX Assessing whether a patient is afflicted with ovarian cancer, useful in

assessing the stage or progression of the disease, comprises comparing
the expression level of a cancer marker in a sample from a patient and
from a non cancer patient.

XX